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AUG 11 2003

TECH CENTER 1600
DATE: 08/11/2003
TIME: 11:59 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/936,271B

Input Set : A:\MTS3USAseqlist.txt

Output Set: N:\CRF4\07302003\I936271B.raw

3 <110> APPLICANT: Yousef, George M.
 4 Diamandis, Eleftherios
 6 <120> TITLE OF INVENTION: Novel Human Kallikrein-Like Genes
 8 <130> FILE REFERENCE: MTS3USA
 10 <140> CURRENT APPLICATION NUMBER: US 09/936,271B
 11 <141> CURRENT FILING DATE: 2001-09-10
 13 <150> PRIOR APPLICATION NUMBER: PCT/CA00/00258
 14 <151> PRIOR FILING DATE: 2000-03-09
 16 <150> PRIOR APPLICATION NUMBER: US 60/124,260
 17 <151> PRIOR FILING DATE: 1999-03-11
 19 <150> PRIOR APPLICATION NUMBER: US 60/127,386
 20 <151> PRIOR FILING DATE: 1999-04-01
 22 <150> PRIOR APPLICATION NUMBER: US 60/144,919
 23 <151> PRIOR FILING DATE: 1999-07-21
 25 <160> NUMBER OF SEQ ID NOS: 96
 27 <170> SOFTWARE: PatentIn version 3.2
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 4740
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Homo sapiens
 34 <400> SEQUENCE: 1

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39	gctgccagcc ccttctggc ccccaaccac tgcctggta gagttgaggc agcctgagag	180
41	attttagctg gaagtttgcg gcacctgacc ccttggAACAC atccccctggg ggcaggccag	240
43	cccaggctga ggtatgttat aagccccaaag gaggcccctg cggaggcagc aggctggagc	300
45	tcagccccagc agtggaatcc aggagccccag aggtggccgg gtaagaggcc tgggtgtccc	360
47	ccactaaaag cctgcagtgt tcatgatcca actctcccta cagctccatg tcgctggatt	420
49	ctcagcctct gtgccttctg tctccacatc tctctagaca gatctctcac tgtctctagt	480
51	taggagtacat tgcctctagt taggggtctc tctgtctctc tgaatctata tctccatgtc	540
53	taactctcag actgtctctg aggatatctc tcaagcactc tgtctctccg gctctgattc	600
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57	cagatggcta gatgctttct ctaaactttc ctttctacatc agttctctct ctctctcttt	720
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67	ggggctgggtt cctggggta ctcatcctt gttgcgcagg tatctgagta tgcgtgtgt	1020
69	tgtctgtccg tgcttggggg cacagtgttt gttaatgttc aggtgtgact cagtgccctc	1080
71	ttgcttgcg ctgcaaaagct gcctgtgaga cggtaccgtg ttatccgtcc gccatggctg	1140
73	tgcctctgca actccttgc tgcgtgtaaa ttgtgtgtg gcagtgtgcc tgggtgtgt	1200
75	gttgcgttg tgagactctg acagttgtg cctctgaata tctggtgag tgacaacagt	1260
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83	tgtggcttgg	tgtgactgtg	ggcaaggctg	ggagaggata	ggagtgactc	ggcgaggac	1500
85	cgaactcttg	agcatcagtc	tgcgcagaca	agtgaccga	tccttgcctc	cagaacaac	1560
87	tccacccccc	gagcttaat	tcaccccgaa	ggaccggatc	ctaccgctat	gagcctagac	1620
89	tcctctgttg	aaccctcct	gaccgtggct	ttgcaccgct	atggcaccag	tctcacctcc	1680
91	agagctcacc	ccagagccct	gactccgccc	cagaagccct	ggtcccacct	tctgagactg	1740
93	cctctagcca	taacccagct	cttgaagct	tgatggcgcc	cctgcgctgt	aaccccaacc	1800
95	ctaggagcac	tgatcccgc	ttctcagccc	accccccattc	cctgactctc	ctcccaggag	1860
97	ccctgactac	cctgaatccc	tgaccaggt	cctgcaccgt	gatcaccgccc	cctgggagcc	1920
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105	gagccctggg	cccgccctct	gagcccggtc	ccagccctga	ctccgccccg	aggagccctg	2160
107	actgctcctg	aacctctgac	cacgccccctg	ctcggttaagg	ccaccccccag	gaaccctggg	2220
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119	gaaggctctg	ggaggaggac	ggaatgagcc	tggatccggg	gagcccaagag	ggaagggctg	2580
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141	gcagaatgcc	taccgtctg	cagtgcgtga	acgtgtcggt	ggtgtctgag	gaggtctgca	3240
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145	agaaggactc	ctgcaacgtg	agagagggaa	aaggggaggg	caggcgactc	aggaaagggt	3360
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153	cacatagaaa	tgcagttgac	cttccaacag	catggggcct	gagggcggtg	acctccaccc	3600
155	aatagaaaat	cctcttataa	cttttgactc	cccaaaaacc	tgactagaaa	tagctactg	3660
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163	tataagtgg	cttgcgtact	tcaaaccagg	gttggtaag	ggtcaactgt	gtacccagag	3900
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167	tctacaaaga	ggctggcag	ggtggctcat	gcctgtatc	ccagcactt	gggaggcgag	4020
169	gcaggcagat	cacttgaggt	aaggagttca	agaccgcct	ggccaaaatg	gtgaaatcct	4080
171	gtctgtacta	aaaatacaaa	agttagctgg	atatggtg	aggcgcctgt	aatcccagct	4140
173	acttgggagg	ctgaggcagg	agaattgtt	gaatatggg	ggcagaggtt	gaagtgtgtt	4200
175	gagatcacac	cactatactc	cagctgggc	aacagagtaa	gactctgtct	caaaaaaaaaaa	4260

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Input Set : A:\MTS3USAseqlist.txt

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 179 gagacaaagg agagacagac aaacagaaac agacagacca caagcccaag agaagcagcc 4380
 181 agcattcagg acataggaca tcgggaagca ggatttagatg aagttaggaa tctggaatgg 4440
 183 gacttccaac agatatgtt ctggctatg ttgttattga tgatggatct gtctttgttt 4500
 185 ctcagtctca ttttagttct ttctgagccc atatccattt ccacctctct gtgtttgaa 4560
 187 ttctgactct ccctctctt acaacaggg gactctgggg ggccctgtat ctgcaacggg 4620
 189 tacttgagg gccttgtgtc tttcgaaaaa gccccgtgtg gccaagttgg cgtgccaggt 4680
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 205 Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu
 206 20 25 30
 209 Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala
 210 35 40 45
 213 Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser
 214 50 55 60
 217 Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu
 218 65 70 75 80
 221 Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu
 222 85 90 95
 225 Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg
 226 100 105 110
 229 Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu
 230 115 120 125
 233 Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Glu Leu Thr Gly Arg Met
 234 130 135 140
 237 Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val
 238 145 150 155 160
 241 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
 242 165 170 175
 245 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
 246 180 185 190
 249 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
 250 195 200 205
 253 Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
 254 210 215 220
 257 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
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 262 <211> LENGTH: 254
 263 <212> TYPE: PRT
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272	Leu	Gly	Val	Ala	Gly	Ser	Leu	Val	Ser	Gly	Ser	Cys	Ser	Gln	Ile	Ile
273								20		25						30
276	Asn	Gly	Glu	Asp	Cys	Ser	Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu
277								35		40						45
280	Val	Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln
281								50		55						60
284	Trp	Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly
285								65		70						80
288	Leu	Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met
289								85		90						95
292	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu
293								100		105						110
296	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu
297								115		120						125
300	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala
301								130		135						140
304	Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg
305	145							145		150						160
308	Met	Pro	Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu	Glu
309								165		170						175
312	Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe	Cys
313								180		185						190
316	Ala	Gly	Gly	Gly	Gln	Asp	Gln	Lys	Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly
317								195		200						205
320	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly
321								210		215						220
324	Lys	Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu
325	225							225		230						240
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342	tttcggaaaa	gccccgtgtg	gccaagttgg	cgtgccaggt	gcctacacca	acctctgcaa										180
344	attcactgag	tggatagaga	aaaccgtcca	ggccagttaa	ctctggggac	tggaaaccca										240
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Input Set : A:\MTS3USAseqlist.txt
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364 <213> ORGANISM: Artificial
366 <220> FEATURE:
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369 <400> SEQUENCE: 6
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374 <211> LENGTH: 21
375 <212> TYPE: DNA
376 <213> ORGANISM: Artificial
378 <220> FEATURE:
379 <223> OTHER INFORMATION: primer
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388 <213> ORGANISM: Artificial
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391 <223> OTHER INFORMATION: primer
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403 <223> OTHER INFORMATION: primer
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415 <223> OTHER INFORMATION: primer
417 <400> SEQUENCE: 10
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423 <212> TYPE: DNA
424 <213> ORGANISM: Artificial
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433 <210> SEQ ID NO: 12

RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,15,16,17,18,19,20,24,25,26,27,28,29,30,31,32,33,34,35
Seq#:36,37,38,39,40,41,42,46,47,48,49,50,51,52,53,54,55,61,62,63,64,90

VERIFICATION SUMMARY

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